Aleksandar Milosavljevic

List of Publications by Year
in descending order

49 papers	11,158 citations	201674 27 h-index	243625 44 g-index
57 all docs	57 docs citations	57 times ranked	26564 citing authors

#	Article	IF	Citations
1	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	27.8	5,653
2	The NIH Roadmap Epigenomics Mapping Consortium. Nature Biotechnology, 2010, 28, 1045-1048.	17.5	1,705
3	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. Nature Biotechnology, 2010, 28, 1097-1105.	17.5	647
4	Performance of ACMG-AMP Variant-Interpretation Guidelines among Nine Laboratories in the Clinical Sequencing Exploratory Research Consortium. American Journal of Human Genetics, 2016, 98, 1067-1076.	6.2	432
5	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
6	An integrative variant analysis suite for whole exome next-generation sequencing data. BMC Bioinformatics, 2012, 13, 8.	2.6	252
7	exRNA Atlas Analysis Reveals Distinct Extracellular RNA Cargo Types and Their Carriers Present across Human Biofluids. Cell, 2019, 177, 463-477.e15.	28.9	228
8	Proinflammatory Role for let-7 MicroRNAS in Experimental Asthma. Journal of Biological Chemistry, 2010, 285, 30139-30149.	3.4	222
9	ReadDepth: A Parallel R Package for Detecting Copy Number Alterations from Short Sequencing Reads. PLoS ONE, 2011, 6, e16327.	2.5	193
10	The Extracellular RNA Communication Consortium: Establishing Foundational Knowledge and Technologies for Extracellular RNA Research. Cell, 2019, 177, 231-242.	28.9	152
11	exceRpt: A Comprehensive Analytic Platform for Extracellular RNA Profiling. Cell Systems, 2019, 8, 352-357.e3.	6.2	118
12	Glioma-Derived miRNA-Containing Extracellular Vesicles Induce Angiogenesis by Reprogramming Brain Endothelial Cells. Cell Reports, 2020, 30, 2065-2074.e4.	6.4	105
13	Intermediate DNA methylation is a conserved signature of genome regulation. Nature Communications, 2015, 6, 6363.	12.8	91
14	Allele-specific epigenome maps reveal sequence-dependent stochastic switching at regulatory loci. Science, 2018, 361, .	12.6	87
15	Epigenomic Deconvolution of Breast Tumors Reveals Metabolic Coupling between Constituent Cell Types. Cell Reports, 2016, 17, 2075-2086.	6.4	84
16	Genomic Hypomethylation in the Human Germline Associates with Selective Structural Mutability in the Human Genome. PLoS Genetics, 2012, 8, e1002692.	3.5	80
17	Epigenomic footprints across 111 reference epigenomes reveal tissue-specific epigenetic regulation of lincRNAs. Nature Communications, 2015, 6, 6370.	12.8	77
18	ClinGen Pathogenicity Calculator: a configurable system for assessing pathogenicity of genetic variants. Genome Medicine, 2017, 9, 3.	8.2	59

#	Article	IF	Citations
19	Pash 3.0: A versatile software package for read mapping and integrative analysis of genomic and epigenomic variation using massively parallel DNA sequencing. BMC Bioinformatics, 2010, 11, 572.	2.6	48
20	Integration of extracellular RNA profiling data using metadata, biomedical ontologies and Linked Data technologies. Journal of Extracellular Vesicles, 2015, 4, 27497.	12.2	48
21	ClinGen Allele Registry links information about genetic variants. Human Mutation, 2018, 39, 1690-1701.	2.5	48
22	Untargeted metabolomic profiling reveals multiple pathway perturbations and new clinical biomarkers in urea cycle disorders. Genetics in Medicine, 2019, 21, 1977-1986.	2.4	47
23	CDKN2D-WDFY2 Is a Cancer-Specific Fusion Gene Recurrent in High-Grade Serous Ovarian Carcinoma. PLoS Genetics, 2014, 10, e1004216.	3.5	41
24	Evidenceâ€based assessments of clinical actionability in the context of secondary findings: Updates from ClinGen's Actionability Working Group. Human Mutation, 2018, 39, 1677-1685.	2.5	34
25	Guidelines for cell-type heterogeneity quantification based on a comparative analysis of reference-free DNA methylation deconvolution software. BMC Bioinformatics, 2020, 21, 16.	2.6	34
26	Discovering simple DNA sequences by the algorithmic significance method. Bioinformatics, 1993, 9, 407-411.	4.1	33
27	Emerging patterns of epigenomic variation. Trends in Genetics, 2011, 27, 242-250.	6.7	33
28	Extending gene ontology in the context of extracellular RNA and vesicle communication. Journal of Biomedical Semantics, 2016, 7, 19.	1.6	24
29	Histoepigenetic analysis of HPV- and tobacco-associated head and neck cancer identifies both subtype-specific and common therapeutic targets despite divergent microenvironments. Oncogene, 2019, 38, 3551-3568.	5.9	20
30	Epigenetic and senescence markers indicate an accelerated ageing-like state in women with preeclamptic pregnancies. EBioMedicine, 2021, 70, 103536.	6.1	20
31	Designing new microsatellite markers for linkage and population genetic analyses in rhesus macaques and other nonhuman primates. Genomics, 2006, 88, 706-710.	2.9	16
32	ClinGen advancing genomic dataâ€sharing standards as a GA4GH driver project. Human Mutation, 2018, 39, 1686-1689.	2.5	15
33	Clinical diagnosis of metabolic disorders using untargeted metabolomic profiling and disease-specific networks learned from profiling data. Scientific Reports, 2022, 12, 6556.	3.3	15
34	Pooled genomic indexing of rhesus macaque. Genome Research, 2005, 15, 292-301.	5.5	14
35	Testicular germ cell tumors arise in the absence of sex-specific differentiation. Development (Cambridge), 2021, 148, .	2.5	12
36	Effective Aspirin Treatment of Women at Risk for Preeclampsia Delays the Metabolic Clock of Gestation. Hypertension, 2021, 78, 1398-1410.	2.7	10

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37	CTD: An information-theoretic algorithm to interpret sets of metabolomic and transcriptomic perturbations in the context of graphical models. PLoS Computational Biology, 2021, 17, e1008550.	3.2	8
38	MPAPASS software enables stitched multiplex, multidimensional EV repertoire analysis and a standard framework for reporting bead-based assays. Cell Reports Methods, 2022, 2, 100136.	2.9	8
39	Putting epigenome comparison into practice. Nature Biotechnology, 2010, 28, 1053-1056.	17.5	7
40	Histoepigenetic analysis of the mesothelin network within pancreatic ductal adenocarcinoma cells reveals regulation of retinoic acid receptor gamma and AKT by mesothelin. Oncogenesis, 2020, 9, 62.	4.9	5
41	Enabling Atlas2 personal genome analysis on the cloud. , 2011, , .		3
42	Confounding by Repetitive Elements and CpG Islands Does Not Explain the Association between Hypomethylation and Genomic Instability. PLoS Genetics, 2013, 9, e1003333.	3.5	3
43	A community approach to the cancer-variant-interpretation bottleneck. Nature Cancer, 2022, 3, 522-525.	13.2	3
44	Buffy Coat DNA Methylation Profile Is Representative of Methylation Patterns in White Blood Cell Types in Normal Pregnancy. Frontiers in Bioengineering and Biotechnology, 2021, 9, 782843.	4.1	1
45	Comparative analysis for mapping and sequence assembly. , 2005, , .		0
46	ClinGen curation tools, web services and repository for clinical actionability assertions and supporting evidence. Molecular Genetics and Metabolism, 2021, 132, S121-S122.	1.1	0
47	Clinical Evaluation of a Custom Genome Wide 44K Oligoarray for Copy Number Changes in Acute Myeloid Leukemia. Blood, 2008, 112, 4869-4869.	1.4	0
48	Abstract PO-115: Effects of mesothelin exert on tumor microenvironment in pancreatic ductal adenocarcinoma. , 2021, , .		0
49	Abstract PO-004: Basal-like, Classical A, and Classical B subtypes of pancreatic cancer show distinct immuno-suppressive molecular profiles. , 2021, , .		0